

FIGURE 1

CGGACGCGTG GGGACCCATACTTGCTGGTCTGATCCATGCACAAGGCGGGGCTGCTAGGCCTC
TGTGCCCCGGGCTTGGAATTCGGTGCGGATGGCCAGCTCCGGGATGACCCGCCGGGACCCGCT
CGCAAATAAGGTGGCCCTGGTAACGGCCTCCACCGACGGGATCGGCTTCGCCATCGCCCCGGC
GTTTGGCCCAGGACGGGGCCCATGTGGTCGTCAGCAGCCGGAAGCAGCAGAATGTGGACCAG
GCGGTGGCCACGCTGCAGGGGGAGGGGCTGAGCGTGACGGGCACCGTGTGCCATGTGGGGAA
GGCGGAGGACCGGGAGCGGCTGGTGGCCACGGCTGTGAAGCTTCATGGAGGTATCGATATCC
TAGTCTCCAATGCTGCTGTCAACCCTTTCTTTGGAAGCATAATGGATGTCACTGAGGAGGTG
TGGGACAAGACTCTGGACATTAATGTGAAGGCCCCAGCCCTGATGACAAAGGCAGTGGTGCC
AGAAATGGAGAAACGAGGAGGCGGCTCAGTGGTGATCGTGTCTTCCATAGCAGCCTTCAGTC
CATCTCCTGGCTTCAGTCCTTACAATGTCAAGTAAACAGCCTTGCTGGGCCTGACCAAGACC
CTGGCCATAGAGCTGGCCCCAAGGAACATTAGGGTGAAGTGCCTAGCACCTGGACTTATCAA
GACTAGCTTCAGCAGGATGCTCTGGATGGACAAGGAAAAAGAGGAAAGCATGAAAGAAACCC
TGCGGATAAGAAGGTTAGGCGAGCCAGAGGATTGTGCTGGCATCGTGTCTTTCTGTGCTCT
GAAGATGCCAGCTACATCACTGGGGAAACAGTGGTGGTGGGTGGAGGAACCCCGTCCCGCCT
CTGAGAGACCGGGAGACAGCCACAGGCCAGAGTTGGGCTCTAGCTCCTGGTGCTGTTCTGCTG
ATTCACCCACTGGCCTTTCCACCTCTGCTCACCTTACTGTTACCTCATCAAATCAGTTCT
GCCCTGTGAAAAGATCCAGCCTTCCCTGCCGTCAAGGTGGCGTCTTACTCGGGATTCTGCT
GTTGTTGTGGCCTTGGGTAAAGGCCTCCCCTGAGAACACAGGACAGGCCTGCTGACAAGGCT
GAGTCTACCTTGGCAAAGACCAAGATATTTTTTCTGGGCCACTGGTGAATCTGAGGGGTGA
TGGGAGAGAAGGAACCTGGAGTGGAAGGAGCAGAGTTGCAAATTAACAGCTTGCAAATGAGG
TGCAAATAAAATGCAGATGATTGCGCGGCTTTGAAAAAAAAA

FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35672

><subunit 1 of 1, 278 aa, 1 stop

><MW: 29537, pI: 8.97, NX(S/T): 1

MHKAGLLGLCARAWNSVRMASSGMTRRDPLANKVALVTASTDGIGFAIARRLAQDGAHVVS
SRKQQNVNDQAVATLQGEGLSVTGTVCHVGKAEDRERLVATAVKLHGGIDILVSNAAVNPFFG
SIMDVTEEVWDKTL DINV KAPALMTKAVVPEMEKRGGGSVVIVSSIAAFSPSPGFSPYNVSK
TALLGLTKTLAIELAPRNIRVNC LAPGLIKTSFSRMLWMDKEKEESMKETLRIRRLGEPEDC
AGIVSFLCSEDASYITGETVVVGGGTPSRL

Important features of the protein:

Signal peptide:

amino acids 1-15

N-glycosylation site.

amino acids 183-186

N-myristoylation sites.

amino acids 43-48, 80-85, 191-196, 213-218, 272-277

Microbodies C-terminal targeting signal.

amino acids 276-278

10046-19701

FIGURE 3

GCGCCCTGAGCTCCGCCTCCGGGCCCGATAGCGGCATCGAGAGCGCCTCCGTCGAGGACCAGGCGGGCG
CAGGGGGCCGGCGGGCGAAAGGAGGATGAGGGGGCGCAGCAGCTGCTGACCCTGCAGAACCAGGTGGC
GCGGCTGGAGGAGGAGAACCAGACTTTCTGGCTGCGCTGGAGGACGCCATGGAGCAGTACAACTGC
AGAGCGACCGGCTGCGTGAGCAGCAGGAGGAGATGGTGGAACTGCGGCTGCGGTTAGAGCTGGTGC GG
CCAGGCTGGGGGGGCTGCGGCTCCTGAATGGCCTGCCTCCCGGGTCTTTGTGCCTCGACCTCATAC
AGCCCCCTGGGGGGTGCCACGCCCATGTGCTGGGCATGGTGGCGCCTGCCTGCCTCCCTGGAGATG
AAGTTGGCTCTGAGCAGAGGGGAGAGCAGGTGACAAATGGCAGGGAGGCTGGAGCTGAGTTGCTGACT
GAGGTGAACAGGCTGGGAAGTGGCTCTTCAGCTGCTTCAGAGGAGGAAGAGGAGGAGGAGGAGCGCC
CAGGCGACCTTACACCTGCGCAGAAATAGGATCAGCAACTGCAGTCAGAGGGCGGGGGCACGCCAG
GGAGTCTGCCAGAGAGGAAGGGCCAGAGCTTTGCCTTGAGGAGTTGGATGCAGCCATTCCAGGGTCC
AGAGCAGTTGGTGGGAGCAAGGCCGAGTTCAGGCCCGCCAGGTCCCCCTGCCACAGCCTCAGAGTG
GCGGCTGGCCAGGCCCAGCAGAAGATCCGGGAGCTGGCTATCAACATCCGCATGAAGGAGGAGCTTA
TTGGCGAGCTGGTCCGCACAGGAAAGGCAGCTCAGGCCCTGAACCGCCAGCACAGCCAGCGTATCCGG
GAGCTGGAGCAGGAGGCAGAGCAGGTGCGGGCCGAGCTGAGTGAAGGCCAGAGGCAGCTGCGGGAGCT
CGAGGGCAAGGAGCTCCAGGATGCTGGCGAGCGGTCTCGGCTCCAGGAGTTCCGCAGGAGGGTCTGTG
CGGCCCAGAGCCAGGTGCAGGTGCTGAAGGAGAAGAAGCAGGCTACGGAGCGGCTGGTGTCACTGTGCG
GCCAGAGTGAGAAGCGACTGCAGGAGCTCGAGCGGAACGTGCAGCTCATGCGGCAGCAGCAGGGACA
GCTGCAGAGGCGGCTTCGCGAGGAGACGGAGCAGAAGCGGCGCCTGGAGGCAGAAATGAGCAAGCGGC
AGCACCGCGTCAAGGAGCTGGAGCTGAAGCATGAGCAACAGCAGAAGATCCTGAAGATTAAGACGGAA
GAGATCGCGGCCCTTCAGAGGAAGAGGCGCAGTGGCAGCAACGGCTCTGTGGTCAGCCTGGAACAGCA
GCAGAAGATTGAGGAGCAGAAGAAGTGGCTGGACCAGGAGATGGAGAAGGTGCTACAGACGCGGGG
CGCTGGAGGAGCTGGGGGAGGAGCTCCACAAGCGGGAGGCCATCCTGGCCAAGAAGGAGGCCCTGATG
CAGGAGAAGACGGGGCTGGAGAGCAAGCGCCTGAGATCCAGCCAGGCCCTCAACGAGGACATCGTGCG
AGTGTCCAGCCGGCTGGAGCACCTGGAGAAGGAGCTGTCCGAGAAGAGCGGGCAGCTGCGGCAGGGCA
GCGCCCAGAGCCAGCAGCAGATCCGCGGGGAGATCGACAGCCTGCGCCAGGAGAAGGACTCGCTGCTC
AAGCAGCGCCTGGAGATCGACGGCAAGCTGAGGCAGGGGAGTCTGCTGTCCCCGAGGAGGAGCGGAC
GCTGTTCCAGTTGGATGAGGCCATCGAGGCCCTGGATGCTGCCATTGAGTATAAGAATGAGGCCATCA
CATGCCGCCAGCGGTGCTTCGGGCCCTCAGCCTCGTTGCTGTCCAGTGCGAGATGAACCTCATGGCC
AAGCTCAGCTACCTCTCATCTCAGAGACCAGAGCCCTCCTCTGCAAGTATTTTGACAAGGTGGTGAC
GCTCCGAGAGGAGCAGCACCAGCAGCAGATTGCCTTCTCGGAACCTGGAGATGCAGCTGGAGGAGCAGC
AGAGGCTGGTGTACTGGCTGGAGGTGGCCCTGGAGCGGCAGCGCCTGGAGATGGACCGCCAGCTGACC
CTGCAGCAGAAGGAGCACGAGCAGAACATGCAGCTGCTCCTGCAGCAGAGTCGAGACCACCTCGGTGA
AGGGTTAGCAGACAGCAGGAGGCAGTATGAGGCCCGGATTCAAGCTCTGGAGAAGGAACCTGGGCCGTT
ACATGTGGATAAACCAGGAACCTGAAACAGAAGCTCGGCGGTGTGAACGCTGTAGGCCACAGCAGGGGT
GGGAGAAGAGGAGCCTGTGCTCGGAGGGCAGACAGGCTCCTGGAAATGAAGATGAGCTCCACCTGGC
ACCCGAGCTTCTCTGGCTGTCCCCCTCACTGAGGGGGCCCCCGCACCCGGGAGGAGACGCGGGGACT
TGGTCCACGCTCCGTTACCTTGACCTGGAAACGCTCGAGCCTGTGTGGTGAGGAGCAGGGGTCCCCC
GAGGAACCTGAGGCAGCGGGAGGCGGCTGAGCCCCCTGGTGGGGCGGGTGCTTCCTGTGGGTGAGGCAGG
CCTGCCCTGGAACCTTTGGGCCCTTTGTCCAAGCCCCGGCGGGAACCTGCGACGAGCCAGCCCGGGGATGA
TTGATGTCCGGAAAAACCCCTGTAAAGCCCTCGGGGCAGACCCCTGCCTTGAGGGGAGACTCCGAGCCT
GCTGAAAGGGGCAGCTGCCTGTTTTGCTTCTGTGAAGGGCAGTCCTTACCGCACACCCTAAATCCAGG
CCCTCATCTGTACCCTCACTGGGATCAACAAATTTGGGCCATGGCCAAAAGAACTGGACCCTCATTT
AACAAAATAATATGCAAATTCACACCACTTACTTCCATGAAGCTGTGGTACCCAATTGCCGCTTGTG
TCTTGCTCGAATCTCAGGACAATTCTGGTTTCAGGCGTAAATGGATGTGCTTGTAGTTTCAGGGGTTTG
GCCAAGAATCATCACGAAAGGCTCGGTGGCAACCAGGTTGTGGTTTAAATGGTCTTATGTATATAGGG
GAAACTGGGAGACTTTAGGATCTTAAAAAACCATTTAATAAAAAAAATCTTTGAAGGGAC

1003467-12304

FIGURE 4

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465

<subunit 1 of 1, 830 aa, 1 stop

<MW: 95029, pI: 8.26, NX(S/T): 2

MEQYKLQSDRLREQQEEMVELRLRLLELVRPGWGGLRLLNGLPPGSFVPRPHTAPLGGAHAHV
LGMVPPACLPGDEVGSEQRGEQVTNGREAGAEELLTEVNRLGSGSSAASEEEEEEEEEPPRRTL
HLRRNRISNCSQRAGARPGSLPERKGPCLCLEELDAAI PGSRVGGSKARVQARQVPPATAS
EWRLAQAAQKIRELAINIRMKEELIGELVRTGKAAQALNRQHSQRIRELEQEAEQVRAELSE
GQRQLRELEGKELQDAGERSRLQEFRRRVAAAQSQVQLKEKKQATERLVSLSAQSEKRLQE
LERNVQLMRQQQGQLQRRLREETEQRRLLEAEMSKRQHRVKELELKHEQQQKILKIKTEEIA
AFQRKRRSGSNGSVVSLEQQQKIEEQKKWLDQEMEKVLQQRRALEELGEELHKREAILAKKE
ALMQEKTGLESKRLRSSQALNEDIVRVSSRLEHLEKELSEKSGQLRQGSAAQSQQQIRGEIDS
LRQEKDSSLKQRLEIDGKL RQGSLLSPEEERTLFQLDEAIEALDAAIEYKNEAITCRQRVLR
ASASLLSQCEMNLMAKLSYLSSETRAL LCKYFDKVVT LREEQHQQQIAFSELEMQLLEEQQR
LVYWLEVALERQRLEMDRQLTLQQKEHEQNMQLLLQQRDHLGEGGLADSR RQYEARIQALEK
ELGRYMWINQELKQKLGGVNAVGH SRGGEKRS LCSEGRQAPGNEDELHLAPELLWLSPLTEG
APRTREETRDLVHAPLPLTWKRSSLCGEEQGSPEELRQREAAEPLVGRVLPVGEAGLPWNFG
PLSKPRRELRRASPGMIDVRKNPL

Important features:

Leucine zipper pattern.

amino acids 557-579, 794-815

N-glycosylation sites.

amino acids 133-136, 383-386

Kinesin related protein Kif-4 Coiled-coil domain:

amino acids 231-672

FIGURE 5

ATTCTCCTAGAGCATCTTTGGAAGCATGAGGCCACGATGCTGCATCTTGGCTCTTGTCTGCT
GGATAACAGTCTTCCTCCTCCAGTGTTCAAAGGAACTACAGACGCTCCTGTTGGCTCAGGA
CTGTGGCTGTGCCAGCCGACACCCAGGTGTGGGAACAAGATCTACAACCCTTCAGAGCAGTG
CTGTTATGATGATGCCATCTTATCCTTAAAGGAGACCCGCCGCTGTGGCTCCACCTGCACCT
TCTGGCCCTGCTTTGAGCTCTGCTGTCCCGAGTCTTTTGGCCCCCAGCAGAAGTTTCTTGTG
AAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCACCTTATCTCCCATCTCCCGGAGCTGTAC
CAGGAACAGGAGGCACGTCTGTACCCATTAAAAACCCAGGCTCCACTGGCAGACGGCAGAC
AAGGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAACTTCGGAGAGAAGCA
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTTGGAGAGGAGCCCAGCTGGGGATGGC
CAGACTTCAGGGGAAGAATGCCTTCCTGCTTCATCCCCTTTCCAGCTCCCCTTCCCGCTGAG
AGCCACTTTCATCGGCAATAAAATCCCCCACATTTACCATCT

10224300

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA57700

><subunit 1 of 1, 125 aa, 1 stop

><MW: 14198, pI: 9.01, NX(S/T): 1

MRPRCCILALVCWITVFLQCSKGTTDAPVGSGLWLCQPTPRCGNKIYNPSEQCCYDDAILS
LKETRRCGSTCTFWPCFELCCPESFGPQQKFLVKLRVLGMKSQCHLSPIRSCTRNRRHVLYP

Important features:

Signal sequence

amino acids 1-21

N-myristoylation sites.

amino acids 33-39, 70-76

FIGURE 6

FIGURE 7

CCCACGCGTCCGCCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCT
TTTCCCTCCGACGCGCCACGGCTGCCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCG
AACCCCTCCGCGGAGAGGAGCGAGGCGGCGCCAGGGTGGCCCCCGGGGCGCGCTTGGTCTCG
GAGAAGCGGGGACGAGGCCGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTT
GGGGCCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCCG
GTGTGCGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTTAGTGGTCCGCCCCACGCGGG
TCGCCGGCCGGCCCAGGATGGGCGCTGGCAACCCGGGCCCCGCGCCCGCGCTGCTACCCCTG
CGCCCGCTGCGAGCCCGGCGTCCGGCCCCGCGCCCTGCGCTCATGGACGGCGGCTCCCGGCTG
GCGGCGGCGCGCCCCCGGGCTGTGAATGCGACTCGCCCCCTCGGCCGCGCTCCCCGCCCGCCC
GCCCGCCGGGACGTGGTAGGGGATGCCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCA
GTTCCCTCCTGGTCACCTGCTGCCTGATGGTGGCTCTGTGCAGTCCGAGCATCCCGCTGGAG
AAGCTGGCCCAGGCACCAGAGCAGCCGGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGG
CCCGGGGCGGGTGAACGAGCTCGGGCGCCCGGCGAGGGACGAGGGCGGCAGCGGCCGGGACT
GGAAGAGCAAGAGCGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCC
TGGGTCTCCAGGGCGGGGGCGCCAAGGCCGGGGATCTGCAGGTCCGGCCCCGCGGGGACAC
CCCGCAGGCGGAAGCCCTGGCCGAGCCGCCAGGACGCGATTGGCCCCGGAACTCGCGCCCCA
CGCCCGAGCCACCCGAGGAGTACGTGTACCCGGACTACCGTGGCAAGGGCTGCGTGGACGAG
AGCGGCTTCGTGTACGCGATCGGGGAGAAGTTCGCGCCGGGCCCCCTCGGCCTGCCCGTGCCCT
GTGCACCGAGGAGGGGGCCGCTGTGCGCGCAGCCCGAGTGCCCGAGGCTGCACCCGCGCTGCA
TCCACGTGACACGAGCCAGTGCTGCCCCGAGTGCAAGGAGAGGAAGAACTACTGCGAGTTC
CGGGGCAAGACCTATCAGACTTTGGAGGAGTTCGTGGTGTCTCCATGCGAGAGGTGTCGCTG
TGAAGCCAACGGTGAGGTGCTATGCACAGTGTGAGCGTGTCCCCAGACGGAGTGTGTGGACC
CTGTGTACGAGCCTGATCAGTGCTGTCCCATCTGCAAAAATGGTCCAAACTGCTTTGCAGAA
ACCGCGGTGATCCCTGCTGGCAGAGAAGTGAAGACTGACGAGTGCACCATATGCCACTGTAC
TTATGAGGAAGGCACATGGAGAATCGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGC
AAATGTAGACGCTTCCCAGAACACAACTCTGACTTTTTCTAGAACATTTTACTGATGTGAA
CATTCTAGATGACTCTGGGAACTATCAGTCAAAGAAGACTTTTGATGAGGAATAATGGAAAA
TTGTTGGTACTTTTCCTTTTCTTGATAACAGTTACTACAACAGAAGGAAATGGATATATTTT
AAAACATCAACAAGAACTTTGGGCATAAAATCCTTCTCTAAATAAATGTGCTATTTTACAG
TAAGTACACAAAAGTACACTATTATATATCAAATGTATTTCTATAATCCCTCCATTAGAGAG
CTTATATAAGTGTTTTCTATAGATGCAGATTAAAAATGCTGTGTTGTCAACCGTCAAAAAA
AAAAAAAAAAAAAAAAAAAA

FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68818

><subunit 1 of 1, 325 aa, 1 stop

><MW: 35296, pI: 5.37, NX(S/T): 0

MPSSTAMAVGALSSSLVTCCLMVALCSPSIPLEKLAQAPEQPGQEKREHATRDGPGRVNEL
GRPARDEGGSGRDWKSksGRGLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDTQPQAEALA
AAAQDAIGPELAPTPEPPPEEYVYPDYRGKGCVDSESGFVYAIGKFAFGPSACPCLCTEEGPL
CAQPECPRLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVSPCERCRCCEANGEVL
CTVSACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIPAGREVKTDECTICHCTYEETWR
IERQAMCTRHECRQM

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 11-30

Glycosaminoglycan attachment site.

amino acids 80-83

N-myristoylation sites.

amino acids 10-15, 102-107, 103-108

Cell attachment sequence.

amino acids 114-117

EGF-like domain cysteine pattern signature.

amino acids 176-187

100345-49936001

FIGURE 9

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCAC
TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG
AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCGTGGGTATGACTGAGA
ACTGCAATAGGAAAGATTTTCTGACCTGTTCATCGGGGGACCACCATTATGACACACGGAAAC
TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTGGTGGGGACAAAAG
GCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG
GTGCTTGTGGCCTCCTATAACCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCCTGTCCCAGGAGACCGGCAGTGTC
CTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
GGCGCCACTCATTGTTATGATGGGTACATTATCTCTCAGGAGGTGGGCTGTCCACCAAAT
GAGCATTCAAGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTTGAACCACACCAGACAAATCG
GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG
GTGGGGAGTGTTTTGCCCTTCCTGCTTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGA
CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGAGACCAGATTCTTTC
CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCA
ACACTGGGGAGAGCCTGGAGCATCCGGACTTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG
GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59847

><subunit 1 of 1, 437 aa, 1 stop

><MW: 46363, pI: 6.22, NX(S/T): 3

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLKSGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLLRGRGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLNCSASSSSVLLN
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVCPSC

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 243-260

N-glycosylation sites.

amino acids 46-49, 189-192, 382-385

Glycosaminoglycan attachment sites.

amino acids 51-54, 359-362

N-myristoylation sites.

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174,
198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352,
360-365, 361-366, 388-393, 408-413, 419-424

FIGURE 11

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCCTG
GCTGCGGGCGCTGCTCTCGTCGCTTGCGCGCTGCTCTCTTCTAGAGCCGAGGGACCCGGTGGC
CTCGTCGCTCAGCCCCCTATTTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTAT
TGTCGGGCCCCGAGGCTCCGTGGCGGGACCCTGAGCTGCTGGAGGGGACCTGCACCCCGGTG
CAGCTGGTCGCCCTCATTCGCCACGGCACCCGCTACCCACGGTCAAACAGATCCGCAAGCT
GAGGCAGCTGCACGGGTTGCTGCAGGCCCGCGGGTCCAGGGATGGCGGGGCTAGTAGTACCG
GCAGCCGCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTGTGGTACGCGGACTGGATGGAC
GGGCAGCTAGTAGAGAAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCT
CTTCCCGGCCCTTTTCAGCCGTGAGAACTACGGCCGCTGCGGCTCATCACCAGTTCCAAGC
ACCGCTGCATGGATAGCAGCGCCGCCCTTCTGCAGGGGCTGTGGCAGCACTACCACCCTGGC
TTGCCGCCCGCCGGACGTGCGAGATATGGAGTTTGGACCTCCAACAGTTAATGATAAACTAAT
GAGATTTTTTGATCACTGTGAGAAGTTTTTAAGTGAAGTAGAAAAAATGCTACAGCTCTTT
ATCACGTGGAAGCCTTCAAACTGGACCAGAAATGCAGAACATTTTAAAAAAGTTGCAGCT
ACTTTGCAAGTGCCAGTAAATGATTTAAATGCAGATTTAATTCAAGTAGCCTTTTTTCACCTG
TTCATTTGACCTGGCAATTAAAGGTGTTAAATCTCCTTGGTGTGATGTTTTTGACATAGATG
ATGCAAAGGTATTAGAATATTTAAATGATCTGAAACAATATTGGAAAAGAGGATATGGGTAT
ACTATTAACAGTCGATCCAGCTGCACCTTGTTTCAGGATATCTTTCAGCACTTGGACAAAGC
AGTTGAACAGAAACAAAGGTCTCAGCCAATTTCTTCTCCAGTCATCCTCCAGTTTGGTCATG
CAGAGACTCTTCTTCCACTGCTTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACA
GCGTACAATTACAAAAACAAATGCATCGGAAGTTCCGAAGTGGTCTCATTTGTACCTTATGC
CTCGAACCTGATATTTGTGCTTTACCACTGTGAAAATGCTAAGACTCCTAAAGAACAAATTCC
GAGTGCAGATGTTATTAAATGAAAAGGTGTACCTTTGGCTTACTCACAGAAACTGTTTCA
TTTTATGAAGATCTGAAGAACCACTACAAGGACATCCTTCAGAGTTGTCAAACCAGTGAAGA
ATGTGAATTAGCAAGGGCTAACAGTACATCTGATGAACTATGAGTAACTGAAGAACATTTTT
AATTCTTTAGGAATCTGCAATGAGTGATTACATGCTTGTAATAGGTAGGCAATTCCTTGATT
ACAGGAAGCTTTTATATTACTTGAGTATTTCTGTCTTTTCACAGAAAAACATTGGGTTTCTC
TCTGGGTTTGGACATGAAATGTAAGAAAAGATTTTTCACTGGAGCAGCTCTCTTAAGGAGAA
ACAAATCTATTTAGAGAAACAGCTGGCCCTGCAAATGTTTACAGAAATGAAATTCTTCCTAC
TTATATAAGAAATCTCACACTGAGATAGAATTGTGATTTCATAATAACACTTGAAAAGTGCT
GGAGTAACAAAATATCTCAGTTGGACCATCCTTAACTTGATTGAACTGTCTAGGAACTTTAC
AGATTGTTCTGCAGTTCTCTCTTTCTCCTCAGGTAGGACAGCTCTAGCATTTTCTTAATC
AGGAATATTGTGGTAAGCTGGGAGTATCACTCTGGAAGAAAGTAACATCTCCAGATGAGAAT
TTGAAACAAGAAACAGAGTGTTGTAAAAGGACACCTTCACTGAAGCAAGTCGGAAAGTACAA
TGAAAATAAATATTTTTGGTATTTATTTATGAAATATTTGAACATTTTTTCAATAATTCCTT
TTTACTTCTAGGAAGTCTCAAAGACCATCTTAAATTATTATATGTTTGGACAATTAGCAAC
AAGTCAGATAGTTAGAATCGAAGTTTTTCAAATCCATTGCTTAGCTAACTTTTTCAATTCTGT
CACTTGGCTTCGATTTTTATATTTTCTATTATATGAAATGTATCTTTTGGTTGTTTGATTT
TTCTTTCTTTCTTTGTAAATAGTTCTGAGTTCTGTCAAATGCCGTGAAAGTATTTGCTATAA
TAAAGAAAATCTTGTGACTTTAAAAA

FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76400

><subunit 1 of 1, 487 aa, 1 stop

><MW: 55051, pI: 8.14, NX(S/T): 2

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSPYFGTKTRYEDVNPVLLS
GPEAPWRDPELLEGTCTPVQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGASSTGS
RDLGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHR
CMDSSAAFLQGLWQHYHPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYH
VEAFKTGPEMQNILKKVAATLQVPVNDLNADLIQVAFFTCSEFDLAIKGVKSPWCDVFDIDDA
KVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAE
TLLPLLSLMGYFKDKEPLTAYNYKKQMHRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRV
QMLLNEKVLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSDEL

Important features:

Signal sequence

amino acids 1-30

N-glycosylation sites.

amino acids 242-246, 481-485

N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

Endoplasmic reticulum targeting sequence.

amino acids 484-489

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2015. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

FIGURE 13

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCTCGACATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAAGTGTCTTGCATCATTACGGATTTCGC
AGACAAGTGACCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGTCTGTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTTATCGCTGTGAGGTCGTTGCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT
CCAGAGCCAATCCAGATTTTCGCAATTTCTTCTTTCCACTTAAACTCTGAAACAGGCACTTTGGTGTTCCTGCTG
TTCACAAGGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGGTTCTGTTGTCTTGTGCTGTACTGGCCCTGA
TCACGTTGGGCATCTGCTGTGCATACAGACGCTGGCTACTTCACTCAACAATAAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAACCAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTG
TGATCTGAGAGCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTCAAGAGCTTTTCGTTTTTGGCCAAAGTTGACCA
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCTCAAGATGGACCCGGTAAATATAACCACAA
GGAAGCGAAACTGGGTGCGTTCCTGAGTTGGGTTCCTAATCTGTTTCTGGCCTGATTCCCGCATGAGTATTAGG
GTGATCTTAAAGAGTTTGTCTACGTAAACGCCCGTGTGGGCCCTGTGAAGCCAGCATGTTTACCCTGGTCTGT
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGCGGGAACCCA
GAAAAGGCTTCTTACACAGCAGCCTTACTTCATCGGCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC
TGATCGGTGTGTGAGTGTCCATTGTGGAGAAGCTTTTGGATCAGCATTTTGTAAAAACAACCAAAATCAGGAAG
GTAATTTGGTTGCTGGAAGAGGGATCTTGCCTGAGGAACCCTGCTTGTCCAACAGGGTGTGAGGATTTAAGGAAA
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTTTATTTTATAAAATTT
TACATCTAAATTTTGTCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAAACTGTAAATATATTGT
CATACAATGTTAAATAACCTATTTTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTTAAAT
TGGAAAAATATCAATAAATTAAGAGTATTTTACCCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTTCTTTCT
CACACAAGTTTTAGCCTTTTTTACAAGGGAACCTACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAAATCCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT
GCCCTTCTTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCGCTCTAGCTACTGTTGCCTCGCTGTCTGCCAGGAGGCCCT
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCAGTGAGCTTTACTCACGTGGCCCTTGTCTCATCCAGCACAGC
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCCAGCTTTGGGCTCCTGTAACAGACCTCT
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTAAAGTTTGTTTAATTATTTGTT
AAGATTGTCTAAGGCCAAAGGCAATGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTTAAAGAAAATGGAT
CCCCTGTTCTCTTTGCCACAGAGAAAGCACCAGAGCCACAGGCTCTGTGCGATTTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTGAGGTGGAGCAGCCAGGTGAAAGGCCTGGCGGGGAGGAAAG
TGAAACGCCCTGAATCAAAAGCAGTTTCTAATTTTGACTTTAAATTTTTCATCCGCCGGAGACACTGCTCCCAT
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
GCCGTGCTGGACTCAGGACTGAAGTGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCTGGA
GAATGGCTCTCACTACTCACCTTGTCTTTTCACTTCCAGTGTCTTGGGTTTTTTTATACTTTGACAGCTTTTTTTT
AATTGCATACATGAGACTGTGTTGACTTTTTTTTAGTTATGTGAAACACTTTGCCGAGGCCGCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGTCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC
CCTCCATCATTTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCTCAGCGTTGGGGATTACGCTCCAGCCTCCT
TCTTGGTTGTATAGTGATAGGGTAGCCTTATTGCCCTCTTCTTATACCCTAAAACCTTCTACACTAGTGCCA
TGGGAACCAGGTCTGAAAAAGTAGAGAGAAGTGAAGTAGACTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACCTGTTATTTTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTTGGCATTGTGTTAAC
CTCATTTATAAAAAGCTTCAAAAAAACCCA

FIGURE 14

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624

><subunit 1 of 1, 310 aa, 1 stop

><MW: 35020, pI: 7.90, NX(S/T): 3

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSCLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDLNIIGGIIGG
VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

biochem. j.

項目	単位	数値
1. 総人口	人	1,234,567
2. 男性人口	人	612,345
3. 女性人口	人	622,222
4. 人口密度	人/平方キロメートル	123.45
5. 出生率	‰	10.5
6. 死亡率	‰	8.2
7. 自然増減率	‰	2.3
8. 出生数	人	12,345
9. 死亡数	人	9,876
10. 人口増加数	人	2,469
11. 人口増加率	％	0.2
12. 人口減少率	％	-0.1
13. 人口変動率	％	0.1
14. 人口変動率	％	0.1
15. 人口変動率	％	0.1
16. 人口変動率	％	0.1
17. 人口変動率	％	0.1
18. 人口変動率	％	0.1
19. 人口変動率	％	0.1
20. 人口変動率	％	0.1
21. 人口変動率	％	0.1
22. 人口変動率	％	0.1
23. 人口変動率	％	0.1
24. 人口変動率	％	0.1
25. 人口変動率	％	0.1
26. 人口変動率	％	0.1
27. 人口変動率	％	0.1
28. 人口変動率	％	0.1
29. 人口変動率	％	0.1
30. 人口変動率	％	0.1
31. 人口変動率	％	0.1
32. 人口変動率	％	0.1
33. 人口変動率	％	0.1
34. 人口変動率	％	0.1
35. 人口変動率	％	0.1
36. 人口変動率	％	0.1
37. 人口変動率	％	0.1
38. 人口変動率	％	0.1
39. 人口変動率	％	0.1
40. 人口変動率	％	0.1
41. 人口変動率	％	0.1
42. 人口変動率	％	0.1
43. 人口変動率	％	0.1
44. 人口変動率	％	0.1
45. 人口変動率	％	0.1
46. 人口変動率	％	0.1
47. 人口変動率	％	0.1
48. 人口変動率	％	0.1
49. 人口変動率	％	0.1
50. 人口変動率	％	0.1
51. 人口変動率	％	0.1
52. 人口変動率	％	0.1
53. 人口変動率	％	0.1
54. 人口変動率	％	0.1
55. 人口変動率	％	0.1
56. 人口変動率	％	0.1
57. 人口変動率	％	0.1
58. 人口変動率	％	0.1
59. 人口変動率	％	0.1
60. 人口変動率	％	0.1
61. 人口変動率	％	0.1
62. 人口変動率	％	0.1
63. 人口変動率	％	0.1
64. 人口変動率	％	0.1
65. 人口変動率	％	0.1
66. 人口変動率	％	0.1
67. 人口変動率	％	0.1
68. 人口変動率	％	0.1
69. 人口変動率	％	0.1
70. 人口変動率	％	0.1
71. 人口変動率	％	0.1
72. 人口変動率	％	0.1
73. 人口変動率	％	0.1
74. 人口変動率	％	0.1
75. 人口変動率	％	0.1
76. 人口変動率	％	0.1
77. 人口変動率	％	0.1
78. 人口変動率	％	0.1
79. 人口変動率	％	0.1
80. 人口変動率	％	0.1
81. 人口変動率	％	0.1
82. 人口変動率	％	0.1
83. 人口変動率	％	0.1
84. 人口変動率	％	0.1
85. 人口変動率	％	0.1
86. 人口変動率	％	0.1
87. 人口変動率	％	0.1
88. 人口変動率	％	0.1
89. 人口変動率	％	0.1
90. 人口変動率	％	0.1
91. 人口変動率	％	0.1
92. 人口変動率	％	0.1
93. 人口変動率	％	0.1
94. 人口変動率	％	0.1
95. 人口変動率	％	0.1
96. 人口変動率	％	0.1
97. 人口変動率	％	0.1
98. 人口変動率	％	0.1
99. 人口変動率	％	0.1
100. 人口変動率	％	0.1

CAGGACCAGGTCCTTCCTACGCTGGAGCAGCGGGGAGACAGCCACCATGCACATCCTCGTGGTCCATGCCATGGTG
 ATCCTGCTGACGCTGGGCCCCGCTCGAGCCGACGACAGCGAGTTCAGGCGCTGCTGGACATCTGGTTTCCGGAG
 GAGAAGCCACTGCCACCGCCTTCCTGGTGGACACATCGGAGGAGGCGCTGCTGCTTCCTGACTGGCTGAAGCTG
 CGCATGATCCGTTCTGAGGTGCTCCGCCCTGGTGGACGCCGCCCTGCAGGACCTGGAGCCGCGAGCAGCTGCTGCTG
 TTCGTGCAGTCTGTTTGGCATCCCCGTGTCCAGCATGAGCAAACCTCCTCCAGTTCCTGGACCAGGCAGTGGCCCA
 GACCCCCAGACTCTGGAGCAGAACATCATGGACAAGAATTACATGGCCCCACCTGGTGGAGGTCCAGCATGAGCGC
 GGCGCCTCCGGAGGCCAGACTTTCCACTCCTTGCTCACAGCCTCCCTGCCGCCCGCCGAGACAGCACAGAGGCCA
 CCCAAACC~~CAA~~AGAGCAGCCCAGAGCAGCCCATAGGCCAGGGCCGGATTTCGGGTGGGGACCCAGCTCCGGGTGCTC
 GGCCCTGAGGACGACCTGGCTGGCATGTTCTCCAGATTTTCCCCTCAGCCCCGACCCCTCGGTGGCAGAGCTCC
 AGTCCCCGCCCGTGGCCCTCGCCCTGCAGCAGGCCCTGGGCCAGGAGCTGGCCCGCGTCTGCCAGGGCAGCCCC
 GAGGTGCCGGGCATCAGGTGCGTGTCTTCGAGGCCCTCGCCACCCTGCTCAGTCCCCACACGGCGGTGCCCTG
 GTGATGTCCATGACACCGTAGCATTCTCTGGCTGGCCCGCTGCTGCGCAGCTGCGCAGTACACAGCAGCTGTGTG
 CCACAGGACACCGGCTTCTCCTCGCTCTTCTCTGAAGTGTCTCTGCAGATGCTGCAGTGGCTGGACAGCCCTGGC
 GTGGAGGGCGGGCCCCCTGCGGGCACAGCTCAGGATGCTTGCCAGCCAGGCCTCAGCCGGGGCGCAGGCTCAGTGAT
 GTGCGAGGGGGGCTCTTGCGCTGGCCGAGGCCCTGGCCTTCCGTGAGGACCTGGAGGTGGTTCAGCTCCACCGTC
 CGTGCCGTTCATCGCCACCTGAGGTCTGGGGAGCAGTGCAGCGTGGAGCCGGACCTGATCAGCAAAGTCTCCAG
 GGGCTGATCGAGGTGAGGTCCCCCACCTGGAGGAGCTGCTGACTGCATTCTTCTCTGCCACTGCGGATGCTGCC
 TCCCCGTTTCCAGCCTGTAAGCCCCGTGTGGTGGTGAGCTCCCTGCTGCTGCAGGAGGAGGAGCCCTGGCTGGG
 GGGAAGCCGGGTGCGGACGGTGGCAGCCTGGAGGCCGTGCGGCTGGGGCCCTCGTCAGGCCTCCTAGTGGACTGG
 CTGGAAATGCTGGACCCCGAGGTGGTTCAGCAGCTGCCCCGACCTGCAGCTCAGGCTGCTCTTCTCCCGAGGAAG
 GGCAAAGGTCAGGCCCAGGTGCCCTCGTTCGTCCCTACCTCCTGACCCTCTTCACGCATCAGTCCAGCTGGCCC
 ACACCTGCACCAGTGCATCCGAGTCTGTGCTGGGCAAGAGCCGGGAACAGAGGTTTCGACCCCTCTGCCTCTCTGGAC
 TTCTCTTGCGCTGCATCCATGTTCTTCGCATCTGGCAGGGGCGGGACCCAGCGCACCCCGCAGAAAGCGGCGGGAG
 GAGCTGGTGTCTGCGGGTCCAGGGCCCGGAGCTCATCAGCCTGGTGGAGCTGATCCTGGCCGAGGCGGAGACGCGG
 AGCCAGGACGGGGACACAGCCGCTGCAGCCTCATCCAGGCCCGGCTGCCCTGCTGCTCAGCTGCTGCTGTGGG
 GACGATGAGAGTGTTCAGGAAGGTGACGGAGCACCTGTGAGGCTGCATCCAGCAGTGGGGAGACAGCGTGTGGGA
 AGGCGCTGCCGAGACCTTCTCTGCAGCTCTACCTACAGCGGCCGAGAGCTGCGGGTCCCCGTGCCTGAGGTCCTA
 CTGCACAGCGAAGGGGTGCCACGAGCAGCAGCTGTGCAAGCTGGACGGACTCATCCACCGCTTCATCAGCTCCTT
 GCGGACACCGAGCACTCCCGGCGTGTGGAGAACCAGGGGGCGGATGCCAGCATGGCCTGCCGGAAGCTGGCGGTG
 GCGCACCCGCTGCTGCTGCTCAGGCACCTGCCCATGATCGCGGCGCTCCTGCACGGCCGCACCCACCTCAACTTC
 CAGGAGTTCCGGCAGCAGAAACCACCTGAGCTGCTTCTTCACAGTGTCTGGGCTGCTGGAGCTGCTGCAGCCGCAC
 GTGTTCCGCAGCGAGCACCAGGGGGCGCTGTGGGACTGCCTTCTGTCTTCATCCGCTGCTGCTGAATTACAGG
 AAGTCTTCCCGCATCTGGCTGCCCTTCATCAACAAGTTTGTGCGAGTTCATCCATAAGTACATTACCTACAATGCC
 CCAGCAGCCATCTCTTCTTCGAGAAGCACGCCGACCCGCTCCACGACCTGTCTTCGACAACAGTGACCTGGTG
 ATGCTGAAATCCCTCTTTCAGGGCTCAGCCTGCCCAGCAGGGACGACAGGACCGACCGAGGCCTGGACGAAGAG
 GGCGAGGAGGAGAGCTCAGCCGGCTCCTTGCCCCCTGGTACGCGTCTCCTGTTCACCCCTCTGACCGCGGCCGAG
 ATGGCCCCCTACATGAAACGGCTTTCGCCGGGGCCAAACGGTGGAGGATCTGCTGGAGGTTCTGAGTGACATAGAC
 GAGATGTCCCGCGGAGACCCGAGATCCTGAGCTTCTTCTCGACCAACCTGCAGCGGCTGATGAGCTCGGCCGAG
 GAGTGTTCGCGCAACCTCGCCTTCAGCCTGGCCCTGCGCTCCATGCAGAAACAGCCCCAGCATTGCAGCCGCTTTC
 CTGCCCACGTTTCATGTACTGCCCTGGGCAGCCAGGACTTTGAGGTGGTGCAGACGGCCCTCCGGAACCTGCCTGAG
 TACGCTCTCTGTGCCAAGAGCACGCGGCTGTGCTGCTCCACCGGGCCTTCTGGTGGGCATGTACGGCCAGATG
 GACCCAGCGCGCAGATCTCCGAGGCCCTGAGGATCCTGCATATGGAGGCCGTGATGTGAGCCTGTGGCAGCCGA
 CCCCCCTCAAGCCCCGGCCGCTCCGCTCCCCGGGGATCCTCGAGGCAAAGCCAGGAAGCGTGGGCGTTGCTGG
 TCTGTCCGAGGAGGTGAGGGCGCCGAGCCTTGAGGCCAGGACCGCCAGGACCAATACTCCGAGCCCTGGGGTGG
 CTCCCGGGCCGGCCGTGGCATCAGGGGCCGTGCCAGCAAGCCCTCATTCACCTTCTGGGCCACAGCCCTGCCGCG
 AGCGGCGGATCCCCCGGGCATGGCCTGGGCTGGTTTTGAATGAAACGACCTGAACTGTCAA

FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77631

><subunit 1 of 1, 1029 aa, 1 stop

><MW: 114213, pI: 6.42, NX(S/T): 0

MHILVVHAMVILLTLGPPRADDSEFQALLDIWFPEEKPLPTAFLVDTSEEALLLPDWLKLRM
IRSEVLRLVDAALQDLEPQQLLLFVQSFGIPVSSMSKLLQFLDQAVAHDPQTLEQNIMDKNY
MAHLVEVQHERGASGGQTFHSLLTASLPPRRDSTEAPKPKSSPEQPIGQGRIRVGTQLRVLG
PEDDLAGMFLQIFPLSPDPRWQSSSPRPVALALQQALGQELARVVQGSPEVPGITVRVLQAL
ATLLSSPHGGALVMSMHRSHFLACPLLRLCQYQRCVPQDTGFSSFLKVLQMLQWLDSFG
VEGGPLRAQLRMLASQASAGRRLSDV RGGLRLAEALAFRQDLEVVSSTVRAVIATLRSGEQ
CSVEPDLISKVLQGLIEVRSPHLEELLTAFFSATADAASFPACKPVVVVSSLLLQEEEP
GGKPGADGGSLEAVRLGPSSGLLVDWLEMLDPEVVSSCPDLQLRLLFSRRKGKGQAQVPSFR
PYLLTLFTHQSSWPTLHQ CIRVLLGKSREQRFDPASLDFLWACIHVPRIWQGRDQRTPOKR
REELVLRVQGP ELISLVELILAE AETRSQDGD TAACSLIQARLPLLLSCCGDDESVRKVTE
HLSGCIQQWGD SVLGRRCDLLQLYLQRP ELRVVP EVLLHSEGAASSSVCKLDGLIHRFI
TLLADTSDSRALENRGADASMACRKLAVAHPLLLLRHLP MIAALLHGRTHLNFQEF RQQNHL
SCFLHVLGLLELLQPHVFRSEHQ GALWDCLLSFIRLLN YRKSSRH LAAFINKFVQFIHKYI
TYNAPAAISFLQKHADPLHDL SFDNSDLV MLKSLLAGLSLPSRDDRTDRGLDEEGEEESSAG
SLPLVSVSLFTPLTAAEMAPYMKRLSRGQTVEDLLEVLS DIDEMSRRRPEILSFFSTNLQRL
MSSAECCRNLA FSLALRSMQNSPSIAAAFLPTFM YCLGSQDFEVVQTALRNLPEYALLCQE
HAAVLLHRAFLVGM YGQMDPSAQISEALRILHMEAVM

Important features:

Signal peptide:

amino acids 1-16

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

N-myristoylation sites.

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449,
665-671, 698-704

Amidation sites.

amino acids 329-333, 634-638

protein 234001

FIGURE 17

CCGGGCCATGCAGCCTCGGCCCGCGGGCGCCCGCCGCGCACCCGAGGAGATGAGGCTCCGC
AATGGCACCTTCCTGACGCTGCTGCTCTTCTGCCTGTGCGCCTTCCTCTCGCTGTCTGGTA
CGCGGCACTCAGCGGCCAGAAAGGCGACGTTGTGGACGTTTACCAGCGGGAGTTCTGGCGC
TGCGCGATCGGTTGCACGCAGCTGAGCAGGAGAGCCTCAAGCGCTCCAAGGAGCTCAACCTG
GTGCTGGACGAGATCAAGAGGGCCGTGTCAGAAAGGCAGGCGCTGCGGAGACGGAGACGGCAA
TCGCACCTGGGGCCGCCTAACAGAGGACCCCCGATTGAAGCCGTGGAACGGCTCACACCGGC
ACGTGCTGCACCTGCCACCGTCTTCCATCACCTGCCACACCTGCTGGCCAAGGAGAGCAGT
CTGCAGCCCGCGGTGCGCGTGGGCCAGGGCCGCACCGGAGTGTCGGTGATGGGCATCCC
GAGCGTGCGGCGGAGGTGCACTCGTACCTGACTGACACTCTGCACTCGCTCATCTCCGAGC
TGAGCCCGCAGGAGAAGGAGGACTCGGTTCATCGTGGTGCTGATCGCCGAGACTGACTCACAG
TACACTTCGGCAGTGACAGAGAACATCAAGGCCTTGTTCCCCACGGAGATCCATTCTGGGCT
CCTGGAGGTCATCTCACCTCCCCCACTTCTACCCTGACTTCTCCCGCTCCGAGAGTCCT
TTGGGGACCCCAAGGAGAGAGTCAGGTGGAGGACCAAACAGAACCTCGATTACTGCTTCCTC
ATGATGTACGCGCAGTCCAAAGGCATCTACTACGTGCAGCTGGAGGATGACATCGTGGCCAA
GCCCAACTACCTGAGCACCATGAAGAACTTTGCACTGCAGCAGCCTTCAGAGGACTGGATGA
TCCTGGAGTTCTCCAGCTGGGCTTCATTGGTAAGATGTTCAAGTCGCTGGACCTGAGCCTG
ATTGTAGAGTTCATTCTCATGTTCTACCGGGACAAGCCCATCGACTGGCTCCTGGACCATAT
TCTGTGGGTGAAAGTCTGCAACCCCGAGAAGGATGCGAAGCACTGTGACCGGCAGAAAGCCA
ACCTGCGGATCCGCTTCAAACCGTCCCTCTTCCAGCACGTGGGCACTCACTCCTCGCTGGCT
GGCAAGATCCAGAACTGAAGGACAAAGACTTTGGAAAGCAGGCGCTGCGGAAGGAGCATGT
GAACCCGCCAGCAGAGGTGAGCACGAGCCTGAAGACATAACAGCACTTCACCTGGAGAAAG
CCTACCTGCGCGAGGACTTCTTCTGGGCCTTCACCCCTGCCGCGGGGGACTTCATCCGCTTC
CGCTTCTTCCAACCTCTAAGACTGGAGCGGTTCTTCTTCCGCAGTGGGAACATCGAGCACCC
GGAGGACAAGCTCTTCAACACGTCTGTGGAGGTGCTGCCCTTCGACAACCCTCAGTCAGACA
AGGAGGCCCTGCAGGAGGGCCGCACCGCCACCCTCCGGTACCCTCGGAGCCCCGACGGCTAC
CTCCAGATCGGCTCCTTCTACAAGGGAGTGGCAGAGGGAGAGGTGGACCCAGCCTTCGGCCC
TCTGGAAGCACTGCGCCTCTCGATCCAGACGGACTCCCTGTGTGGGTGATTCTGAGCGAGA
TCTTCTGAAAAAGGCCGACTAAGCTGCGGGCTTCTGAGGGTACCCTGTGGCCAGCCCTGAA
GCCCACATTTCTGGGGGTGTGCTCACTGCCGTCCCCGGAGGGCCAGATACGGCCCCGCCCAA
AGGGTTCTGCCGTGGCGTCGGGCTTGGGCCGGCCTGGGGTCCGCCGCTGGCCCCGAGGCCCTA
GGAGCTGGTGCTGCCCCCGCCCGCCGGGCCGCGGAGGAGGCAGGCGGCCCCACACTGTGCC
TGAGGCCCGGAACCGTTTCGACCCCGCCTGCCCCAGTCAGGCCGTTTTAGAAAGAGCTTTTAC
TTGGGCGCCCGCCGTCTCTGGCGCGAACACTGGAATGCATATACTACTTTATGTGCTGTGTT
TTTTATTCTTGGATACATTTGATTTTTTTCACGTAAGTCCACATATACTTCTATAAGAGCGTG
ACTTGTAAATAAAGGGTTAATGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA82307

><subunit 1 of 1, 548 aa, 1 stop

><MW: 63198, pI: 8.10, NX(S/T): 4

MRLRNGTFLTLLLFCLCAFLSLSWYAALSGQKGDVVDVYQREFLALRDRHLHAAEQESLKRSK
ELNLVLDEIKRAVSERQALRDGDGNRTWGRLTEDPRLKPWNGSHRHVLHLPTVFFHLLPHLLA
KESSLQPAVRVGQGRGTGVSVMGIPSVRREVHSYLTDTLHSLISELSPQEKEDSVIVVLIAE
TDSQYTSAVTENIKALFPTEIHSGLLLEVISPSPHFYPDFSRRLRESFGDPKERVVRWRTKQNL
YCFLMMYAQSKGIYYVQLEDDIVAKPNYLSTMKNFALQQPSEDWMILEFSQLGFIGKMFKSL
DLSLIVEFILMFYRDKPIDWLLDHILWVKVCNPEKDAKHCDRQKANLRIRFKPSLFQHVGT
SSLAGKIQKLKDKDFGKQALRKEHVNPPAEVSTSLKTYQHFTLEKAYLREDDFFWAFTPAAGD
FIRFRFFQPLRLERFFFRSGNIEHPEDKLFNTSVEVLFPDNPQSDKEALQEGRTATLRYPRS
PDGYLQIGSFYKGVAEGEVDPAFGPLEALRLSIQTDSPVWVILSEIFLKKAD

Important features:

Signal sequence

amino acids 1-23

N-glycosylation sites.

amino acids 5-9, 87-91, 103-107, 465-469

N-myristoylation sites.

amino acids 6-12, 136-142, 370-376, 509-515

1003-164 132701